

FIG. 1

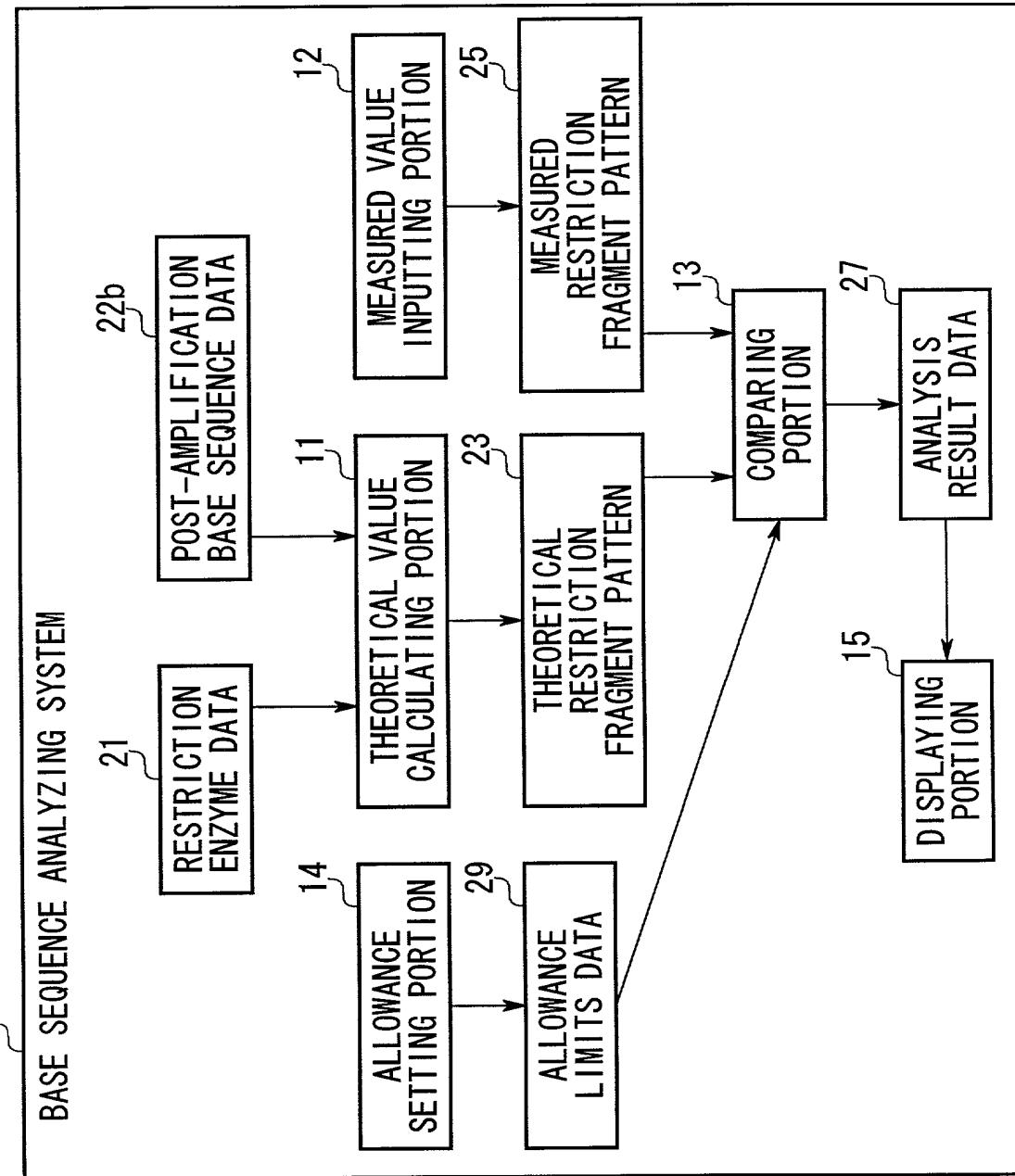


FIG. 2

LOCUS RSP16SRRZ 1490 bp rRNA BCT 04-DEC-1995
DEFINITION Rhodospirillum salexigens 16S ribosomal RNA.
ACCESSION M59070
NID g175871
VERSION M59070.1 GI:175871
KEYWORDS 16S ribosomal RNA.
SOURCE Rhodospirillum salexigens rRNA.
ORGANISM Rhodothalassium salexigens
 Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
 Rhodothalassium.
REFERENCE 1 (bases 1 to 1490)
AUTHORS Woese, C. R.
TITLE A phylogenetic analysis of the some purple bacteria
JOURNAL Unpublished (1991)
FEATURES Location/Qualifiers
source 1..1490
 /organism="Rhodothalassium salexigens"
 /db_xref="taxon:1086"
 /tissue_lib="DSM 2132"
rRNA 1..1490
 /gene="16S rRNA"
 /product="16S ribosomal RNA"
gene 1..1490
 /gene="16S rRNA"
BASE COUNT 342 a 343 c 472 g 284 t 49 others

FIG. 3

ORIGIN

1 gctcagaacg aacgctggcg gcaggcctaa cacatgcaag tcgagcgcac nccttcgggg
61 gtnagcggcg gacgggtgag taacgogtgg gaaacctgctc agggctctgg gataactgct
121 gaaaaacggca gctaataccg gatacggcgt attggaaag aaattcggcc ttggatggc
181 ccgcgttggta ttagcttagat ggtgggtaa cggcctacca tggcgcacat ccatagctgg
241 tttgagagga tgatcagcca cactggact gagacacggc ccagactcct acgggaggca
301 gcagtgggaa atcttagaca atggggcaa ccctgatcta gccatgccgc gtgagtgtatg
361 aaggccttag ggttgtaaag ctcttcagc aggaaagata atgactgtac ctgcagaaga
421 agctccggct aactccgtgc cagcagccgc ggtataacgg agngggcnag cgttgttcgg
481 aattactggg cgtaaagcgc gcgttaggcgg atcggtcagt tgggggtgaa agcccggggc
541 tcaacctcgg aactgccctc aaaactaccg atcnagagtt cggagaggt aagcggaaatt
601 cccagtgtatg aggtgaaatt cgtagatatt gggagaaca ccagtggcga aggccggctta
661 ctggaccgat actgacgctg aggtgcnaaa gcgtggggag caaacaggat tagataccct
721 ggtagtccac gccgtaaacg atgggtgcta gatgtcgggg ctcttagagt ttccgtatcg
781 cagctaacgc attaagcacc ccgcncggg agtacggccg caaggttaaa actcaaagga
841 attgacgggg gcnnngcaca gcggtggagc atgtggttt attcgaanna acgcgcagaa
901 ccttaccagg tcttgacatc ccgggacgac ttccagagat ggatttttc acttcgggtga
961 cccggngaca ggtgctgcat ggctgtcgctc agctcggtc gtgagatgt

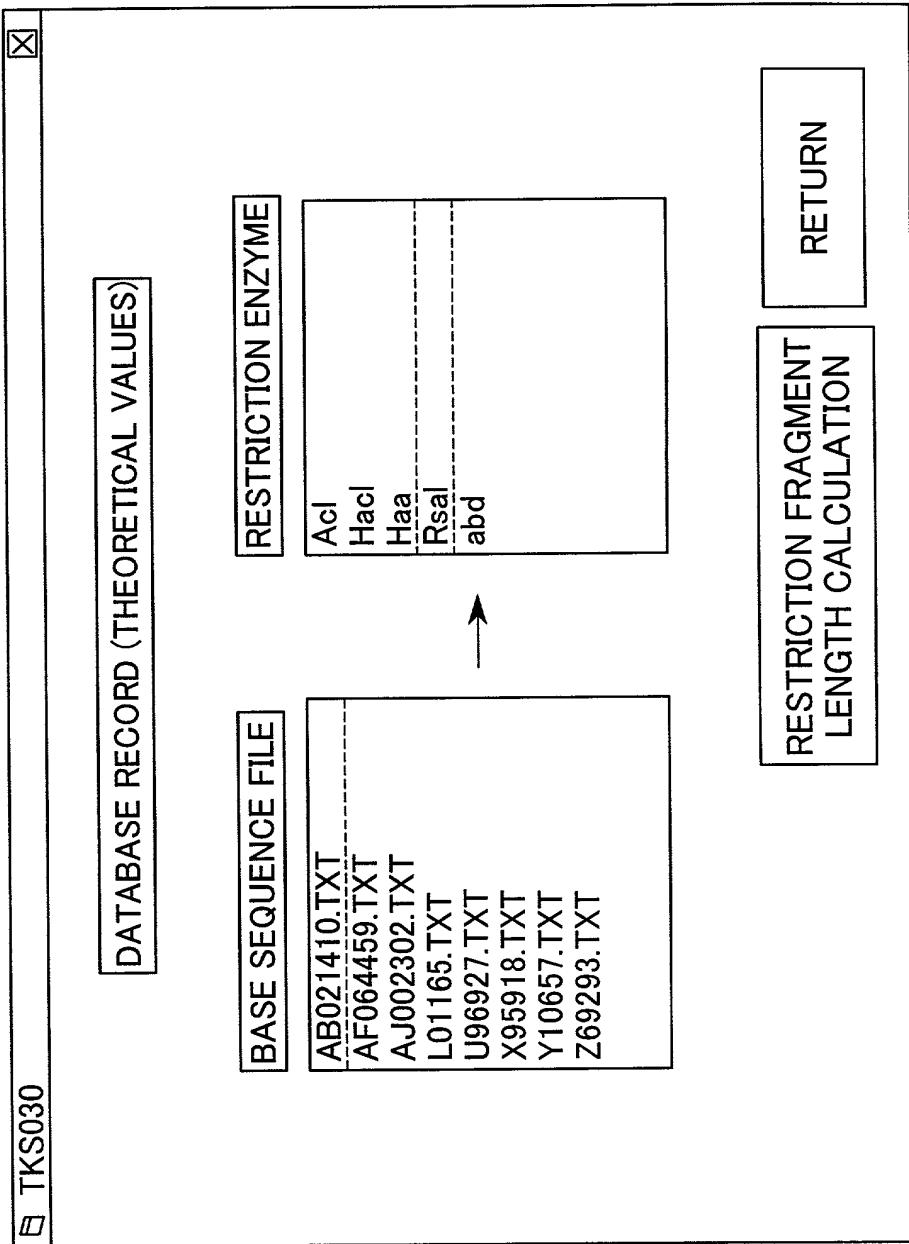
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FIG. 4

RESTRICTION ENZYME DATA

RESTRICTION ENZYME NUMBER	RESTRICTION ENZYME NAME	RECOGNITION SITE	RESTRICTION SITE
1	AluI	agct	2
2	HaeIII	ggcc	2
3	RsaI	gtac	2
4	ScrFI	ccn ^g gg	2
5	HhaI	gcgc	2
6	BamHI	ggatcc	1
7	EcoRI	gaatt	1
8	HindIII	aagctt	1
9	PstI	ctgcag	5
10	PvuII	cagctg	3
11	Sall	gagctc	5
12	SmaI	cccg ^g gg	3
13	XbaI	tctaga	1

FIG. 5



THEORETICAL RESTRICTION FRAGMENT PATTERNS

FIG. 6

DNA NUMBER	NUMERICAL VALUE SECTION	GROUP NAME	NAME OF ORGANISM	NAME OF GENE	RESTRICTION ENZYME NUMBER	RESTRICTION FRAGMENT LENGTH VALUE
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	2	204
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	5	509
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	5	542
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	3	194
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	3	457
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	3	400
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	2	156
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	2	90
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	2	317
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	2	169
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	1	550
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	1	180
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	1	79
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	1	87
AB000278	1		<i>Vibrio iliopiscarius</i>	16S rRNA; 16S ribosomal RNA	2	105
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	2	156
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	5	509
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	5	565
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	4	1074
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	3	194
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	3	234
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	3	223
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	3	423
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	2	90
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	1	175
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	2	204
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	2	317
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	2	105
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	1	236
AB038030	1		<i>Vibrio splendidus</i>	16S ribosomal RNA	1	572

FIG. 7

MEASURED RESTRICTION FRAGMENT PATTERNS

FIG. 8

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SHEET 8 OF 29

DNA NUMBER	NUMERICAL VALUE SECTION	GROUP NAME	NAME OF ORGANISM	NAME OF GENE	RESTRICTION ENZYME NUMBER	MEASURED RESTRICTION FRAGMENT LENGTH VALUE
AP1	2	AP			1	100
AP1	2	AP			1	200
AP1	2	AP			1	300

FIG. 9

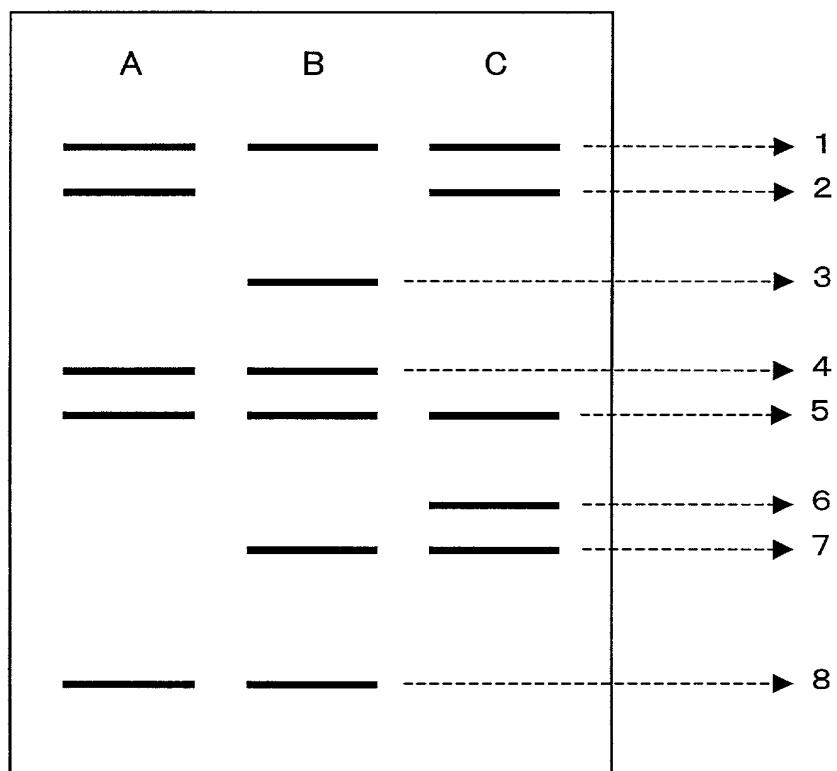


FIG. 10A

	A	B	C	D
A	—	—	—	—
B	0.7	—	—	—
C	0.8	0.5	—	—
D	0.1	0.4	0.3	—

FIG. 10B

$$S(B, A+C) = \frac{S(B, A) + S(B, C)}{2}$$

*1

$$S(D, A+C) = \frac{S(D, A) + S(D, C)}{2}$$

*2

$$S(D, (A+C)+B) = \frac{S(D, A+C) + S(D, B)}{2}$$

*3

	(A+C)+B	D
(A+C)+B	—	—
D	0.3 (*3)	—

FIG. 10C

FIG. 11

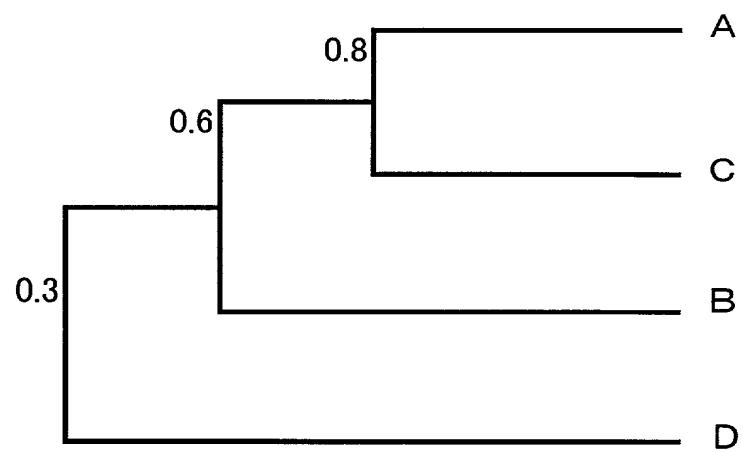


FIG. 12

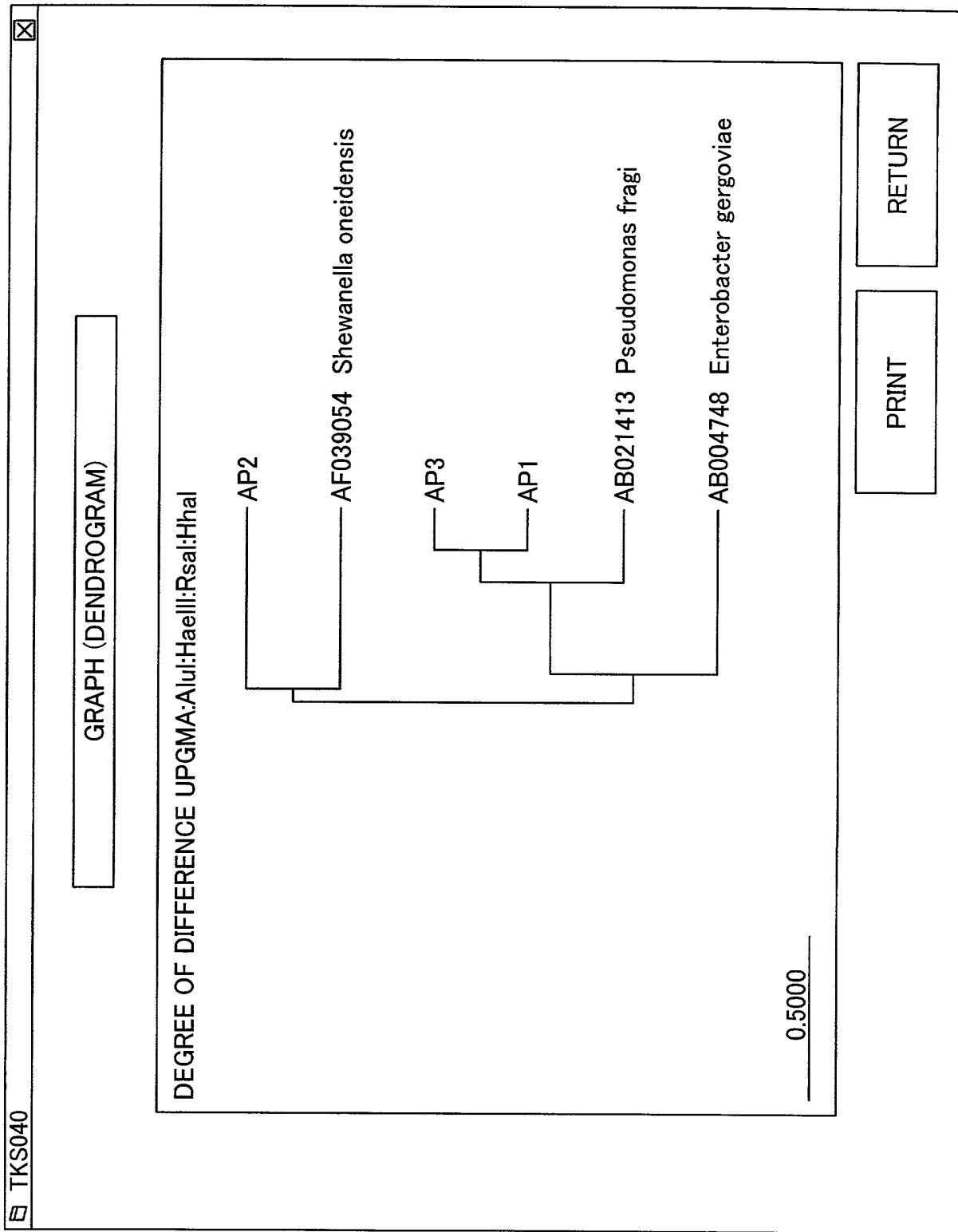


FIG. 13

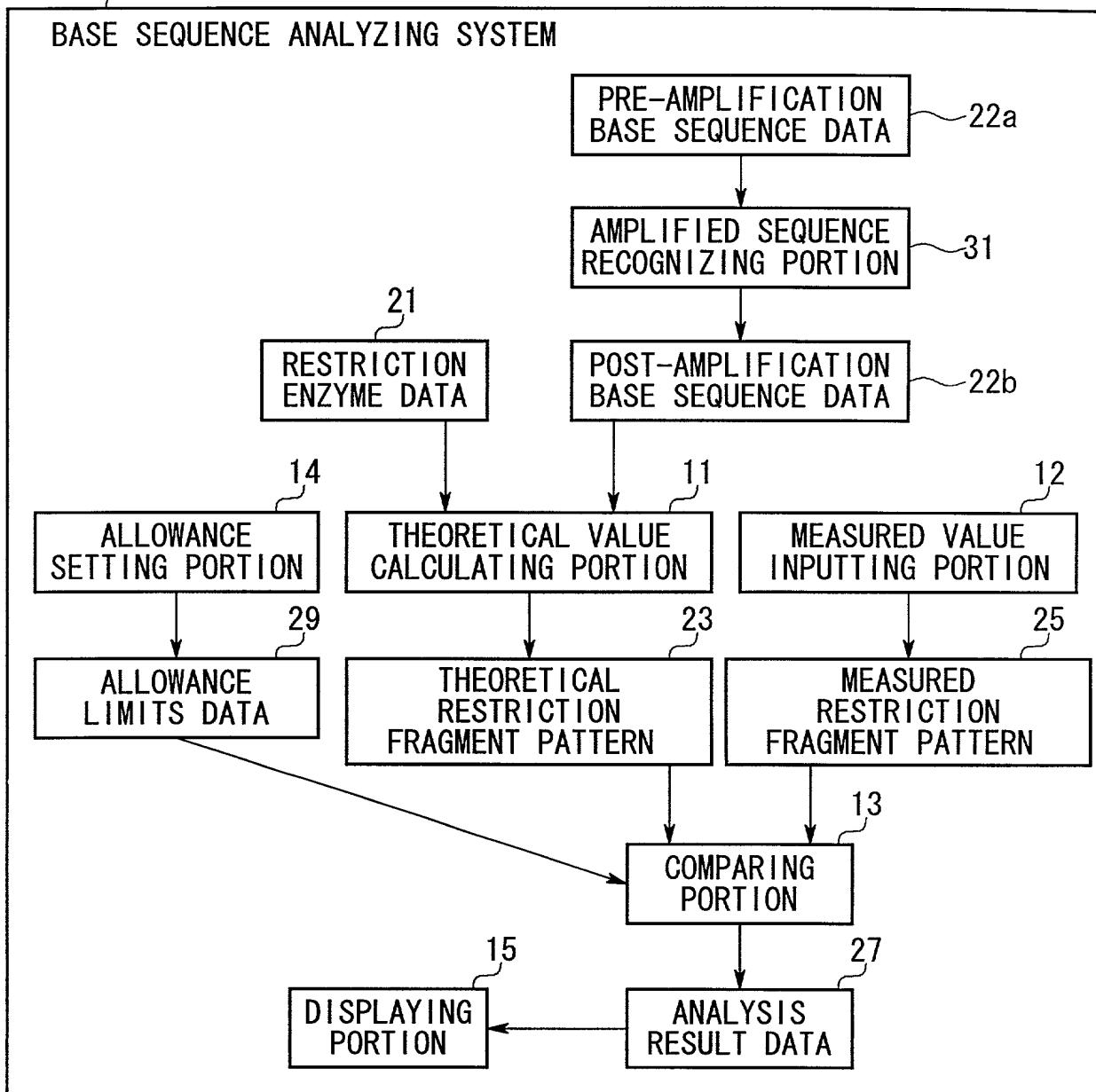


FIG. 14

LOCUS RSP16SRRZ 1490 bp rRNA BCT 04-DEC-1995
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ACCESSION M59070
NID g175871
VERSION M59070.1 GI:175871
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/db_xref="taxon:1086"
/tissue_lib="DSM 2132"
rRNA 1..1490
/gene="16S rRNA"
/product="16S ribosomal RNA"
gene 1..1490
/gene="16S rRNA"
BASE COUNT 342 a 343 c 472 g 284 t 49 others

FIG. 15

ORIGIN

1 ncaacatgag agtttgcattc tggctcagaa cgaacgctgg cggcaggcct aacacatgca
61 agtcgagcgc annccttcg gggtnagcgg cggacgggtg agtaacgcgt gggAACCTGC
121 tcagggctct gggataactg ctggaaacgg cagcttaatac cggatacgcc gtattggaa
181 agaaattcgg ccttggatgg gcccgcgtt gattagctag atggtgggtt aacggcctac
241 catggcgacg atccatagct ggtttgagag gatgatcagc cacactggga ctgagacacg
301 gcccagactc ctacgggagg cagcagtggg gaatctttaga caatggggc aaccctgatc
361 tagccatgcc gcgtgagtga tgaaggcctt agggttgtaa agctcttca gcagggaaaga
421 taatgactgt acctgcagaa gaagctccgg ctaactccgt gccagcagcc gcggtaatac
481 ggagngggcn agcgttgttc ggaattactg ggcgtaaagc gcgcgttaggc ggatcggtca
541 gtgggggtg aaagcccggt gctcaaccctc ggaactgccc tcaaaactac cgatcnagag
601 ttccggagag gtaagcggaa ttccagttt agaggtgaaa ttctgttagata ttgggaagaa
661 caccagtggc gaaggcggct tactggaccg atactgacgc tgaggtgcna aagcgtgggg
721 agcaaacagg attagatacc ctggtagtcc acgcgttaaa cgtatgggtgc tagatgtcgg
781 ggctttaga gtttcggtat cgcagctaac gcattaaagca cccgcncngg ggagtagcgg
841 cgcaaggta aaactcaaag gaattgacgg gggcnngcac aagcggtgga gcatgtggtt
901 taattcgaan naacgcgcag aaccttacca gctttgaca tcccgggacg acttccagag
961 atggatttt tcacttcggt gaccggngt caggtgcgtc atggctgtcg tcagctcggt
1021 tcgtgagatg ttgggttaag tcccnaacg agcgcaccc tcgccttag ttggccagcat
1081 ttgggtgggg actctaaggg aactgcccgt gataagccgg aggaagggtgg ggtatgacgta
1141 aagtccctat ggcctttagt ggctggctt cacacgtgtc acaatggcgg tgacagaggg
1201 cagcggcct gcgagggtga gcgaatctt aaaaaggcgtc tcagttcggt ttgttctgt
1261 caactcgaga gcatgaaggt ggaatcgta gtaatcgccgg atcagcatgc cgcgggtgaat
1321 acgttcccg gnnntgtaca caccggccgt cacaccatgg gagttgggtt gacccgaaga
1381 cggtgagcta acccgaaagg ggggcagnng cccacggtca ggtcagcgcac tggggtnnnn
1441 nngtaacaag nnnnnnnnnn nnnnnnnnnn nnnnngatca cctccttct

11

FIG. 16

SEQUENCE OF FORWARD PRIMER, NAME (ALPHABET OR FIGURE: 5 OR LESS)		
5'	<table border="1"><tr><td>gctcaggatcactggcg: 41f</td></tr></table>	gctcaggatcactggcg: 41f
gctcaggatcactggcg: 41f		
ALLOWANCE LIMITS FOR MISMATCH <input type="text" value="4"/>		
<table border="1"><tr><td>AB00120 AF00232 AF01122 D01255 D01388 D10115 D12303 X12450 X13450 X13451 X80885</td></tr></table>		AB00120 AF00232 AF01122 D01255 D01388 D10115 D12303 X12450 X13450 X13451 X80885
AB00120 AF00232 AF01122 D01255 D01388 D10115 D12303 X12450 X13450 X13451 X80885		
SEQUENCE OF REVERSE PRIMER, NAME (ALPHABET OR FIGURE: 5 OR LESS)		
5'	<table border="1"><tr><td>acatttcacaacacaggatcg: 1066r</td></tr></table>	acatttcacaacacaggatcg: 1066r
acatttcacaacacaggatcg: 1066r		
ALLOWANCE LIMITS FOR MISMATCH <input type="text" value="4"/>		
<table border="1"><tr><td>41f-1066r</td></tr></table>		41f-1066r
41f-1066r		

FIG. 17

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI

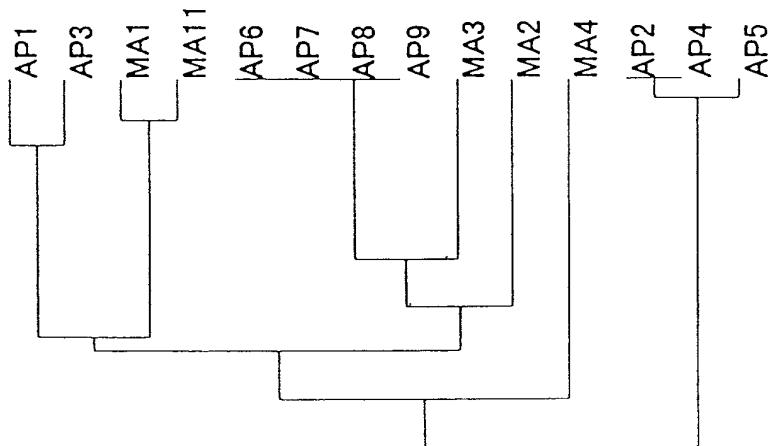


FIG. 18

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI



FIG. 19

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI



FIG. 20

DEGREE OF DIFFERENCE UPGMA:AluI:HaeII:RsaI:HhaI

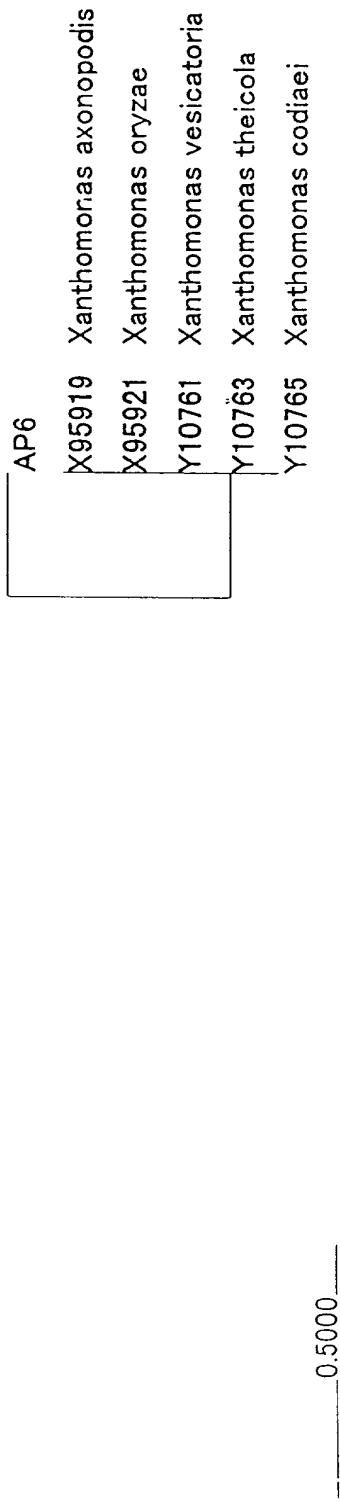
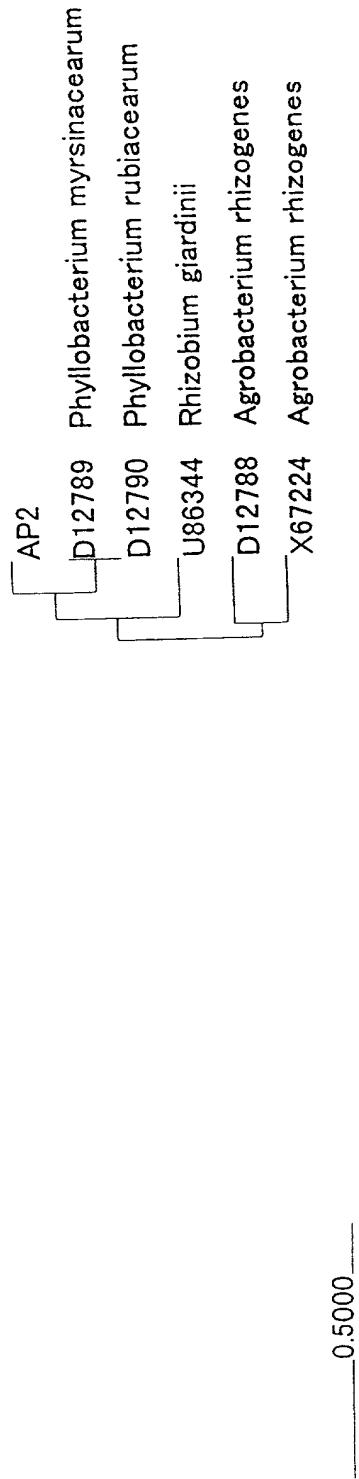


FIG. 21

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI



DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI

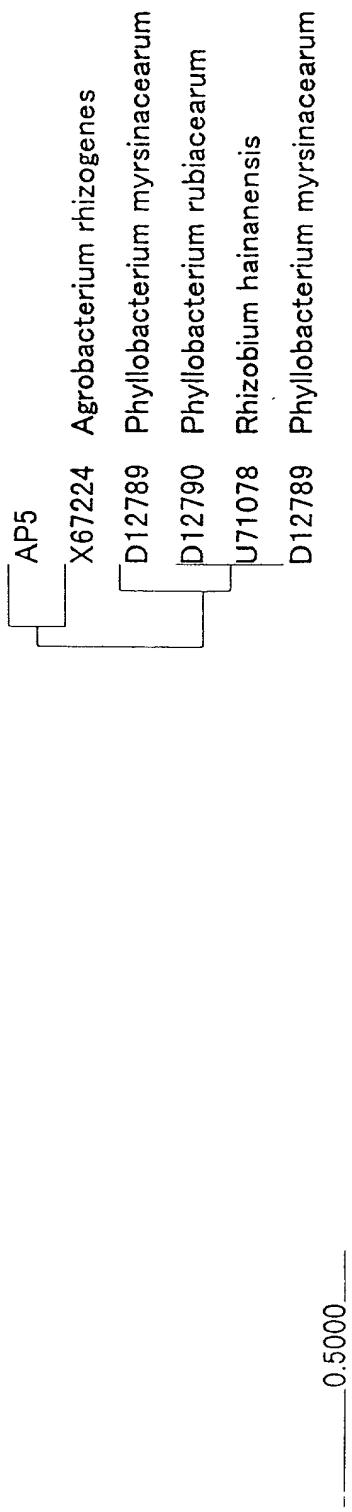
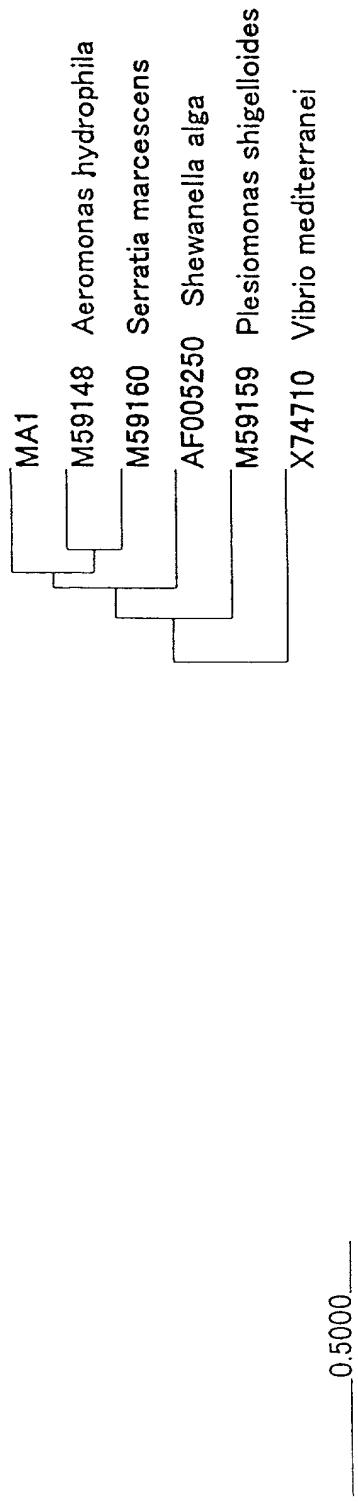


FIG. 23

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI



PTA 3200650

FIG. 24

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI

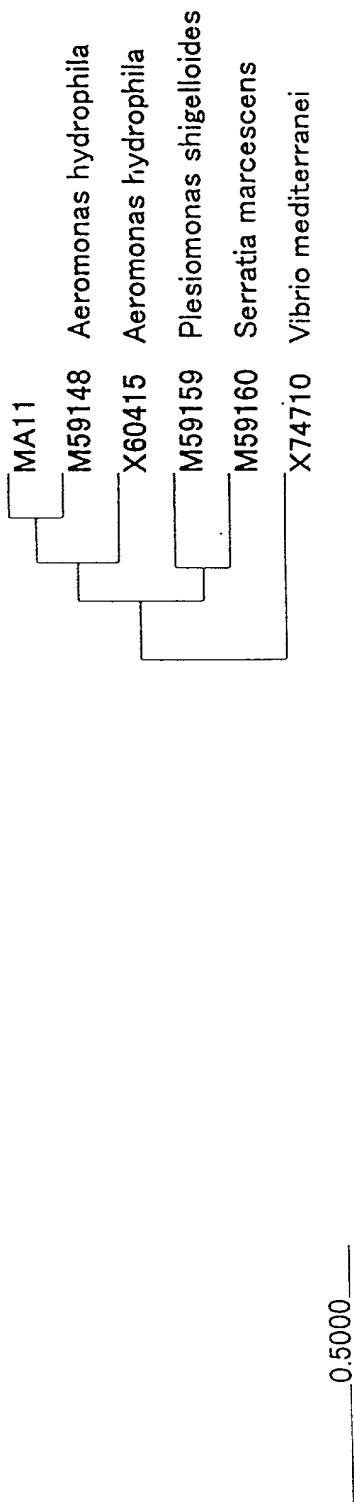


FIG. 25

DEGREE OF DIFFERENCE UPGMA:AluI:HaeII:RsaI:HhaI

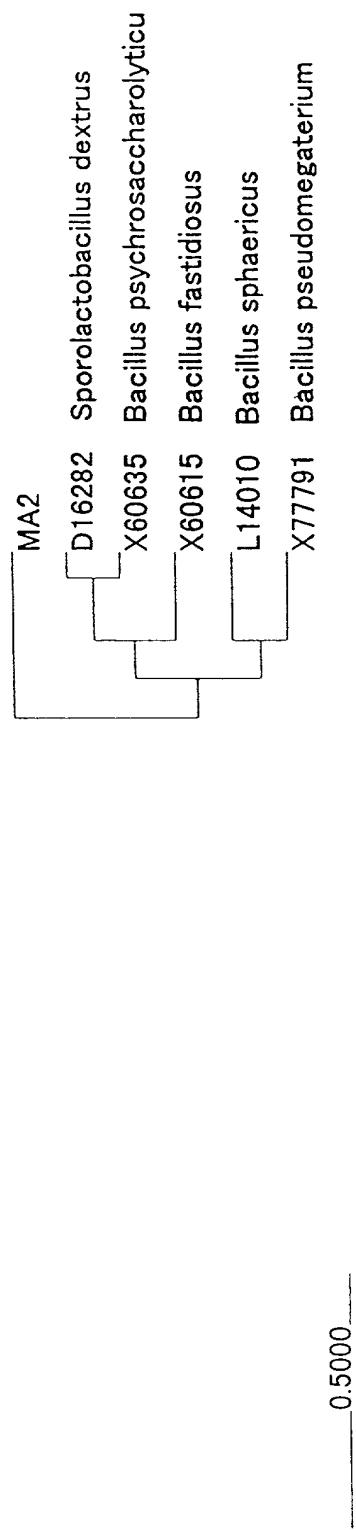


FIG. 26

DEGREE OF DIFFERENCE UPGMA:AluI:HaellI:RsaI:HhaI



FIG. 27

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI

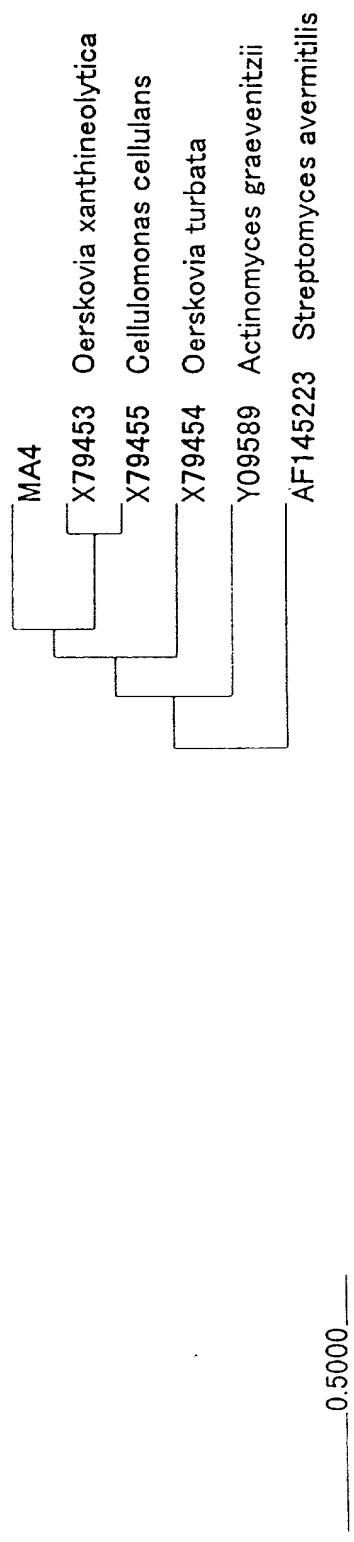


FIG. 28

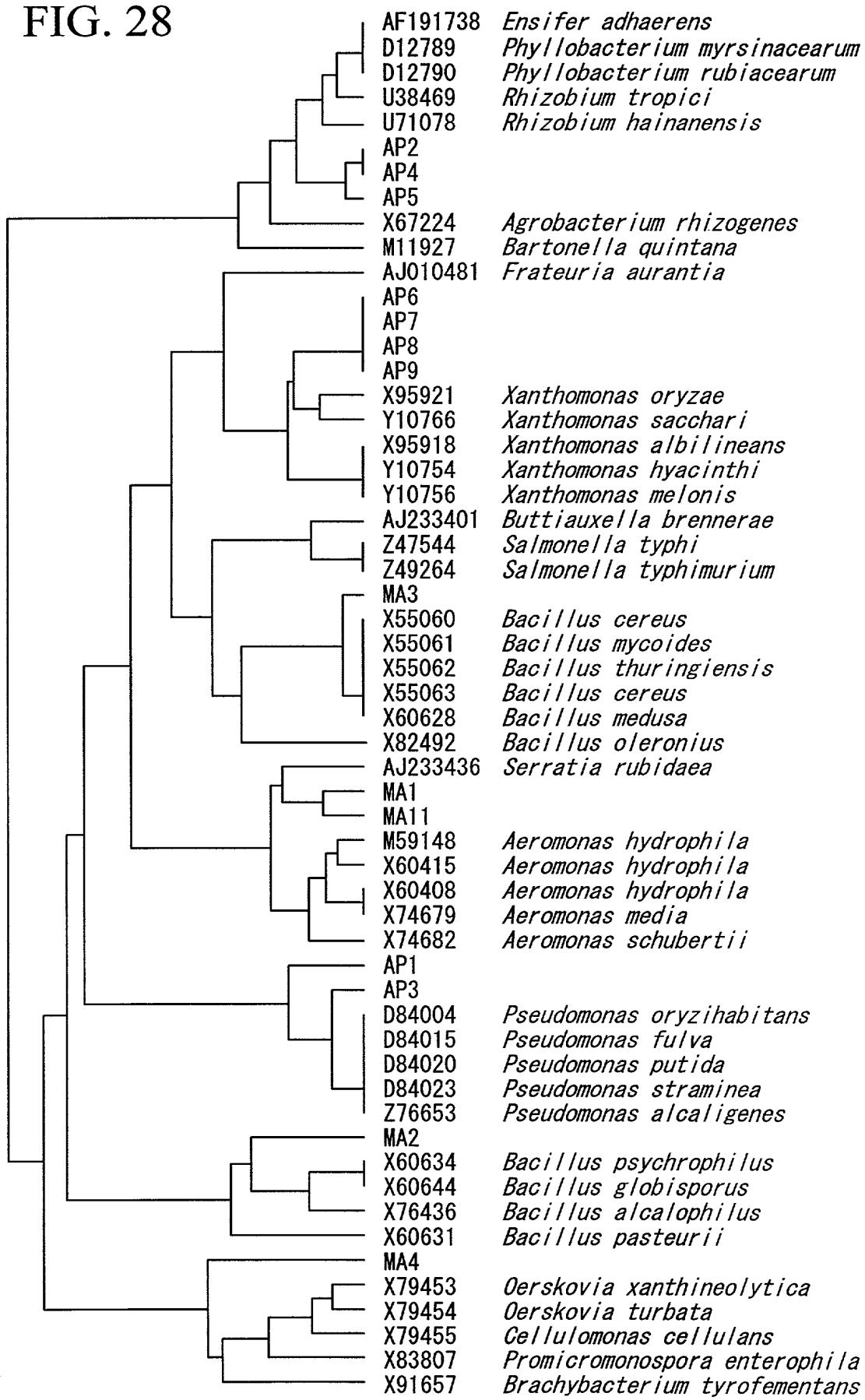


FIG. 29

CLASSIFICATION OF ISOLATED DENITRIFYING BACTERIA by 16S rDNA RFLP (RESTRICTION ENZYME HaeIII, HhaI, AluI, RsaI, SacI) AND COMPARISON OF IDENTIFICATION RESULTS BY HOMOLOGY SEARCH OF BASE SEQUENCES

GROUP	R OF BAC RFLP	BASE SEQUENCE (% HOMOLOGY)
I	20	<i>Enterobacteriaceae</i> <i>Burkholderia</i> genus.
II	9	<i>Klebsiella</i> genus (100%) <i>B. vietnamensis</i> (96.9%, 92.6%, 93.0%, 94.8%, 93.4%), <i>Burkholderia</i> genus (100%)
III+IV	12	<i>Ralstonia</i> genus <i>Ralstonia</i> genus (92.0%, 94.5%, 94.5%), <i>R. paucula</i> (95.1%, 93.8%), <i>R. eutropha</i> (95.6%, 100%, 96.7%)
V	6	<i>Comamonas acidovorans</i> <i>Pseudomonas</i> genus
VI+VII	32	<i>C. acidovorans</i> (98.2%, 100%) <i>P. putida</i> (97.7%, 99.0%, 99.2%), <i>P. fluorescens</i> (95.8%, 99.5%), <i>P. rhodesiae</i> (98.4%)
VII	20	<i>P. putida</i> (100%)
IX	8	<i>P. rhodesiae</i> (98.5%, 99.5%)
X	5	<i>P. stutzeri</i> (98.0%, 94.6%, 92.0%)
XI	3	<i>Acinetobacter haemolyticus</i> (96.1%)
XII	18	<i>Pseudomonas</i> genus
XIII	1	<i>Acidovorax dealfeldii</i> (94.7%)